GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: January 14, 2003, 11:42:22 ; Search time 5.29613 Seconds
(without alignments)
11055.609 Million cell updates/sec

Title: US-09-910-428-2
Perfect score: 26
Sequence: 1 cgtccccaaatcaattacattttctc 26

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002:*
1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
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4: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
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21: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		26	100.0	26	24	ABL57125	Cattle growth horm
c 2		26	100.0	522	24	ABL57128	Cattle growth horm
c 3		26	100.0	540	24	ABL57127	Cattle growth horm
c 4		26	100.0	2869	24	ABL57126	Cattle growth horm
5		19.2	73.8	759	22	AAH31913	Human olfactory re
c 6		19.2	73.8	10433	24	ABL22379	Human immune syste
7		19.2	73.8	611590	21	AAF22303	Arabidopsis thalia
c 8		19	73.1	6591	22	AAS46283	Tumour suppressor
c 9		18.8	72.3	3912	22	AAK78476	Human immune/haema
c 10		18.8	72.3	4322	22	AAK78477	Human immune/haema
c 11		18.8	72.3	17869	24	ABK39921	Human chemically p
c 12		18.8	72.3	17869	24	ABL32105	Human immune syste
c 13		18.6	71.5	371	24	ABK78300	Bacillus clausii g
14		18.6	71.5	628	21	AAF09771	Fusarium venenatum
15		18.6	71.5	2984	23	ABL29546	Drosophila melanog
16		18.2	70.0	311	21	AAZ42644	Human 5' EST isola
c 17		18.2	70.0	394	9	AAN82031	Turkey female-spec
c 18		18.2	70.0	396	24	ABN69419	Streptococcus poly
c 19		18.2	70.0	495	24	ABN69420	Streptococcus poly
c 20		18.2	70.0	708	24	ABK74210	Bacillus lichenifo
c 21		18.2	70.0	785	19	AAV40380	Strawberry structu
c 22		18.2	70.0	6182	24	ABL34015	Human immune syste
c 23		18.2	70.0	32768	20	AAX13065	Enterococcus faeca
24		18.2	70.0	38358	22	AAK73535	Human immune/haema
c 25		18.2	70.0	235033	19	AAV57926	Hereditary haemoch
c 26		18	69.2	501	22	ABA62664	Human foetal liver
c 27		18	69.2	501	22	ABA29974	Probe #8440 for ge
c 28		18	69.2	501	22	AAK11041	Human brain expres
c 29		18	69.2	501	22	AAK36870	Human bone marrow
c 30		18	69.2	501	22	AAI17724	Probe #7657 for ge
c 31		18	69.2	501	22	AAI42664	Probe #11350 used
c 32		18	69.2	501	24	ABS10883	Human genome-deriv
c 33		18	69.2	1450	21	AAC77005	Human ORFX ORF2560
c 34		18	69.2	4398	21	AAC43063	Arabidopsis thalia
c 35		18	69.2	5452	24	ABL33148	Human immune syste
c 36		18	69.2	5875	23	ABL25366	Drosophila melanog
c 37		18	69.2	9893	22	AAK85753	Human immune/haema
c 38		18	69.2	11662	24	ABL33900	Human immune syste
c 39		18	69.2	15270	22	AAK74017	Human immune/haema
c 40		18	69.2	15270	22	AAK85754	Human immune/haema
c 41		18	69.2	18887	24	AAS18543	DNA encoding UDP g
42		18	69.2	25655	22	AAK76405	Human immune/haema
43		18	69.2	143306	24	ABK49586	Human transporter
44		18	69.2	325791	22	AAS43134	Human oestrogen re
45		17.8	68.5	711	21	AAZ45617	DNA encoding a mar

ALIGNMENTS

RESULT 1
ABL57125
ID ABL57125 standard; DNA; 26 BP.
XX
AC ABL57125;
XX
DT 05-AUG-2002 (first entry)
XX
DE Cattle growth hormone receptor gene TG-repeat 3' PCR primer.
XX
KW Cattle, beef, breeding, growth hormone, somatotropin; receptor;
KW microsatellite, marker-assisted selection; PCR; primer; ss.
XX
OS Bos taurus.
XX
PN CA2312269-A1.
XX
PD 20-JAN-2002.
XX
PF 20-JUL-2000; 2000CA-2312269.
XX
PR 20-JUL-2000; 2000CA-2312269.
XX
PA (UMOR) UNIV MISSOURI.
XX
PI Lucy MC, Lubahn DB, Keisler DH, Shibuya H, Johnson GS, Herring WO;
PI Hale CS;
XX
DR WPI; 2002-417707/45.
XX
PT Obtaining head of beef cattle with genetic predisposition for altered
PT carcass weight, by assaying genetic material from head for polymorphism

```
PT   linked to promoter P1 of exon 1A of bovine growth hormone receptor gene
PT
XX
PS   Claim 7; Page 26; 51pp; English.
XX
CC   The present sequence is a primer that is complementary to nucleotides
CC   located 3' to a polymorphic TG-repeat microsatellite located 90 bp
CC   upstream from a major transcription start site in the bovine growth
CC   hormone receptor gene (see ABL57124). The TG-repeat microsatellite
CC   can be used as a genetic marker that correlates with cattle growth.
CC   Cattle having at least 12, and preferably 16-20, copies of the TG
CC   dinucleotide repeat marker show increased carcass weight or weaning
CC   weight compared with cattle having fewer than 12 copies of the TG
CC   dinucleotide repeat. Use of this marker and other genetic markers
CC   in linkage disequilibrium with the locus allows implementation of
CC   selection and breeding schemes for improvement of cattle performance.
CC   Marker-assisted selection with the genetic markers avoids the costly
CC   phenotypic testing associated with traditional breeding schemes.
XX
SQ   Sequence 26 BP; 7 A; 10 C; 0 G; 9 T; 0 other;

  Query Match             100.0%;  Score 26;  DB 24;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 0.097;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CCTCCCCAAATCAATTACATTTCTC 26
           ||||||||||||||||||||||||||
Db       1 CCTCCCCAAATCAATTACATTTCTC 26


RESULT 2
ABL57128/c
ID   ABL57128 standard; DNA; 522 BP.
XX
AC   ABL57128;
XX
DT   05-AUG-2002  (first entry)
XX
DE   Cattle growth hormone receptor gene promoter and exon 1A region.
XX
KW   Cattle; beef; breeding; growth hormone; somatotropin; receptor;
KW   microsatellite; marker-assisted selection; ds.
XX
OS   Bos indicus.
XX
FH   Key             Location/Qualifiers
FT   primer_bind     complement (207..232)
FT                   /*tag= a
FT   satellite       234..255
FT                   /*tag= b
FT                   /note= "TG dinucleotide repeat microsatellite"
FT   primer_bind     275..300
FT                   /*tag= c
FT   exon            344..522
FT                   /*tag= d
FT                   /number= 1A
FT   variation       replace(12,C)
FT                   /*tag= e
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(94,C)
FT                   /*tag= f
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(473,G)
FT                   /*tag= g
FT                   /standard_name= "Single nucleotide polymorphism"
XX
PN   CA2312269 A1.
XX
PD   20-JAN-2002.
XX
PF   20-JUL-2000; 2000CA-2312269.
XX
PR   20-JUL-2000; 2000CA-2312269.
XX
PA   (UMOR ) UNIV MISSOURI.
XX
PI   Lucy MC, Lubahn DB, Keisler DH, Shibuya H, Johnson GS, Herring WO;
PI   Hale CS;
XX
DR   WPI; 2002-417707/45.
XX
PT   Obtaining head of beef cattle with genetic predisposition for altered
PT   carcass weight, by assaying genetic material from head for polymorphism
PT   linked to promoter P1 of exon 1A of bovine growth hormone receptor gene
PT   -
XX
PS   Example 2; Fig 3; 51pp; English.
XX
CC   The present sequence is the promoter and exon 1A region of the
CC   bovine growth hormone receptor gene. A polymorphic TG-repeat
CC   microsatellite located 90 bp upstream from a major transcription
CC   start site in the gene is associated with average weaning weight
CC   and carcass weight of cattle. Cattle having at least 12, and
CC   preferably 16-20, copies of the TG dinucleotide repeat marker
CC   show increased carcass or weaning weight compared with cattle
CC   having fewer than 12 copies of the TG dinucleotide repeat. Use of
CC   this marker and other genetic markers in linkage disequilibrium
CC   with the locus allows implementation of selection and breeding
CC   schemes for improvement of cattle performance. Other genetic
CC   markers may include polymorphisms such as the G/A polymorphic
CC   site in exon 1A. The A allele (found in indicine cattle) contains
CC   a DraI restriction site that is not present in the G allele (found
CC   in taurine cattle). This difference can be used in a PCR/RFLP
CC   assay to distinguish the respective alleles. The 2 T/C upstream
CC   polymorphic sites could similarly be used. Marker-assisted
CC   selection with the genetic markers avoids the costly phenotypic
CC   testing associated with traditional breeding schemes.
XX
SQ   Sequence 522 BP; 124 A; 121 C; 136 G; 141 T; 0 other;

  Query Match             100.0%;  Score 26;  DB 21;  Length 522;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CCTCCCCAAATCAATTACATTTCTC 26
           ||||||||||||||||||||||||||
Db     300 CCTCCCCAAATCAATTACATTTCTC 275


RESULT 3
ABL57127/c
ID   ABL57127 standard; DNA; 540 BP.
XX
AC   ABL57127;
XX
DT   05-AUG-2002  (first entry)
XX
DE   Cattle growth hormone receptor gene promoter and exon 1A region.
XX
KW   Cattle; beef; breeding; growth hormone; somatotropin; receptor;
KW   microsatellite; marker-assisted selection; ds.
XX
OS   Bos taurus.
XX
FH   Key             Location/Qualifiers
FT   primer_bind     complement (207..232)
FT                   /*tag= a
FT   satellite       234..273
FT                   /*tag= b
FT                   /note= "TG dinucleotide repeat microsatellite"
FT   primer_bind     293..318
FT                   /*tag= c
FT   exon            362..540
FT                   /*tag= d
FT                   /number= 1A
FT   variation       replace(12,T)
```

```
FT                   /*tag=  e
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(94,T)
FT                   /*tag=  f
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace(491,A)
FT                   /*tag=  g
FT                   /standard_name= "Single nucleotide polymorphism"
XX
PN   CA2312269-A1.
XX
PD   20-JAN-2002.
XX
PF   20 JUL 2000; 2000CA 2312269.
XX
PR   20-JUL-2000; 2000CA-2312269.
XX
PA   (UMOR ) UNIV MISSOURI.
XX
PI   Lucy MC,  Lubahn DB,  Keisler DH,  Shibuya H,  Johnson GS,  Herring WO;
PI   Hale CS;
XX
DR   WPI; 2002-417707/45.
XX
PT   Obtaining head of beef cattle with genetic predisposition for altered
PT   carcass weight, by assaying genetic material from head for polymorphism
PT   linked to promoter P1 of exon 1A of bovine growth hormone receptor gene
PT   -
XX
PS   Example 2; Fig 3; 51pp; English.
XX
CC   The present sequence is the promoter and exon 1A region of the
CC   bovine growth hormone receptor gene.  A polymorphic TG-repeat
CC   microsatellite located 90 bp upstream from a major transcription
CC   start site in the gene is associated with average weaning weight
CC   and carcass weight of cattle.  Cattle having at least 12, and
CC   preferably 16-20, copies of the TG dinucleotide repeat marker
CC   show increased carcass or weaning weight compared with cattle
CC   having fewer than 12 copies of the TG dinucleotide repeat.  Use of
CC   this marker and other genetic markers in linkage disequilibrium
CC   with the locus allows implementation of selection and breeding
CC   schemes for improvement of cattle performance.  Other genetic
CC   markers may include polymorphisms such as the G/A polymorphic
CC   site in exon 1A.  The A allele (found in indicine cattle) contains
CC   a DraI restriction site that is not present in the G allele (found
CC   in taurine cattle).  This difference can be used in a PCR/RFLP
CC   assay to distinguish the respective alleles.  The 2 T/C upstream
CC   polymorphic sites could similarly be used.  Marker-assisted
CC   selection with the genetic markers avoids the costly phenotypic
CC   testing associated with traditional breeding schemes.
XX
SQ   Sequence 540 BP; 123 A; 123 C; 146 G; 148 T; 0 other;

  Query Match             100.0%;  Score 26;  DB 24;  Length 540;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CCTCCCCAAATCAATTACATTTTCTC 26
           ||||||||||||||||||||||||||
Db     318 CCTCCCCAAATCAATTACATTTTCTC 293


RESULT 4
ABL57126/c
ID   ABL57126 standard; DNA; 2869 BP.
XX
AC   ABL57126;
XX
DT   05-AUG-2002  (first entry)
XX
DE   Cattle growth hormone receptor gene promoter and exon 1A region.
XX
KW   Cattle; beef; breeding; growth hormone; somatotropin; receptor;
KW   microsatellite; marker-assisted selection; ds.
XX
OS   Bos taurus.
XX
FH   Key             Location/Qualifiers
FT   primer_bind     complement (2580..2605)
FT                   /*tag=  a
FT   satellite       2607..2646
FT                   /*tag=  b
FT                   /note= "TG dinucleotide repeat microsatellite"
FT   primer_bind     2666..2680
FT                   /*tag=  c
FT   exon            2735..2869
FT                   /*tag=  d
FT                   /number= 1A
XX
PN   CA2312269-A1.
XX
PD   20-JAN-2002.
XX
PF   20-JUL-2000; 2000CA-2312269.
XX
PR   20-JUL-2000; 2000CA-2312269.
XX
PA   (UMOR ) UNIV MISSOURI.
XX
PI   Lucy MC,  Lubahn DB,  Keisler DH,  Shibuya H,  Johnson GS,  Herring WO;
PI   Hale CS;
XX
DR   WPI; 2002-417707/45.
XX
PT   Obtaining head of beef cattle with genetic predisposition for altered
PT   carcass weight, by assaying genetic material from head for polymorphism
PT   linked to promoter P1 of exon 1A of bovine growth hormone receptor gene
PT   -
XX
PS   Claim 3; Page 41-43; 51pp; English.
XX
CC   The present sequence is the promoter and exon 1A region of the
CC   bovine growth hormone receptor gene.  A polymorphic TG-repeat
CC   microsatellite located 90 bp upstream from a major transcription
CC   start site in the gene is associated with average weaning weight
CC   and carcass weight of cattle.  Cattle having at least 12, and
CC   preferably 16-20, copies of the TG dinucleotide repeat marker
CC   show increased carcass or weaning weight compared with cattle
CC   having fewer than 12 copies of the TG dinucleotide repeat.  Use of
CC   this marker and other genetic markers in linkage disequilibrium
CC   with the locus allows implementation of selection and breeding
CC   schemes for improvement of cattle performance.  Marker-assisted
CC   selection with the genetic markers avoids the costly phenotypic
CC   testing associated with traditional breeding schemes.
XX
SQ   Sequence 2869 BP; 657 A; 640 C; 582 G; 990 T; 0 other;

  Query Match             100.0%;  Score 26;  DB 24;  Length 2869;
  Best Local Similarity   100.0%;  Pred. No. 0.14;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CCTCCCCAAATCAATTACATTTTCTC 26
           ||||||||||||||||||||||||||
Db    2691 CCTCCCCAAATCAATTACATTTTCTC 2666


RESULT 5
AAH31913
ID   AAH31913 standard; DNA; 759 BP.
XX
AC   AAH31913;
XX
DT   30-JUL-2001  (first entry)
XX
DE   Human olfactory receptor polynucleotide, SEQ ID NO: 486.
XX
```

KW Human; olfactory receptor; OR; primary scent determination;
KW secondary scent determination; polypeptide library; odour receptor;
KW scent profile; scent fingerprint; scent representation; ds.
XX
OS Homo sapiens.
XX
PN WO200127158-A2.
XX
PD 19-APR-2001.
XX
PF 06-OCT-2000; 2000WO-US27582.
XX
PR 08-OCT-1999; 99US-0158615.
PR 24-FEB-2000; 2000US-0184809.
XX
PA (DIGI) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
XX
DR WPI; 2001-290713/30.
XX
PT New polynucleotides which encode polypeptides involved in olfactory
PT sensation for identifying olfactory agonists and antagonists
XX
PS Claim 8; Page 375; 1857pp; English.
XX
CC The present sequence is one of a number of isolated polynucleotides
CC which encode polypeptides involved in olfactory sensation. The
CC polynucleotides can be used in screening for olfactory agonists and
CC antagonists. The methods allow for the determination of primary
CC scents and the identification of the odour receptors used to detect
CC these primary scents. The methods also enable determination of
CC secondary scents and the identification of combinations of odour
CC receptors that are involved in detecting such secondary scents.
CC This enables the construction of a scent representation (also called
CC a scent fingerprint or scent profile), which may be used to re-create
CC and edit scents. Libraries of olfactory receptors are useful for
CC determining the interaction pattern of a composition with the receptors,
CC and can be used for determining differences in the olfactory faculties
CC of different individuals.
XX
SQ Sequence 759 BP; 154 A; 210 C; 183 G; 212 T; 0 other;

Query Match 73.8%; Score 19.2; DB 22; Length 759;
Best Local Similarity 87.5%; Pred. No. 89;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CTCCCCAAATCAATTACATTTTCT 25
|||||||||||| || |||||||
Db 323 CTCACCAAATCAATCACTTTTTCT 346

RESULT 6
ABL42379/c
ID ABL42379 standard; DNA; 10433 BP.
XX
AC ABL42379;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human immune system associated gene SEQ ID NO: 352.
XX
KW Human; immune system disease; cytosine methylation; antiasthmatic;
KW antiarteriosclerotic; antianaemic; cytostatic; nootropic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO200200928-A2.
XX
PD 03-JAN-2002.
XX
PF 02-JUL-2001; 2001WO-EP07537.
XX
PR 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2002-130909/17.
XX
PT Nucleic acid comprising fragment of chemically modified gene, useful
PT for diagnosis and treatment of diseases associated with abnormal
PT cytosine methylation
XX
PS Claim 1; SEQ ID NO 352; 32pp + Sequence Listing; German.
XX
CC The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention.
XX
SQ Sequence 10433 BP; 2736 A; 162 C; 2599 G; 4936 T; 0 other;

Query Match 73.8%; Score 19.2; DB 24; Length 10433;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CTCCCCAAATCAATTACATTTTCT 25
|||||||||||| || |||||||
Db 935 CTTCCCAAATAAACTACATTTTCT 912

RESULT 7
AAF22303
ID AAF22303 standard; DNA; 611590 BP.
XX
AC AAF22303;
XX
DT 20-MAR-2001 (first entry)
XX
DE Arabidopsis thaliana chromosome 2 centromere.
XX
KW Centromere; michrosome; vector; ds.
XX
OS Arabidopsis thaliana.
XX
PN WO200055325-A2.
XX
PD 21-SEP-2000.
XX
PF 17-MAR-2000; 2000WO-US07392.
XX
PR 18-MAR-1999; 99US-0125219.
PR 01-APR-1999; 99US-0127409.
PR 18-MAY-1999; 99US-0134770.
PR 13-SEP-1999; 99US-0153584.
PR 17-SEP-1999; 99US-0154603.
XX
PA (UYCH-) UNIV CHICAGO.
XX
PI Preuss D, Copenhaver G, Keith K;
XX
DR WPI; 2000-587529/55.

```
XX
PT   Recombinant DNA construct comprising a plant centromere, useful for
PT   producing stably inherited michrosomes which can serve as vectors for
PT   the construction of transgenic plant and animal cells -
XX
PS   Claim 45; Page 820-959; 1449pp; English.
XX
CC   The present invention relates to a recombinant DNA construct of a plant
CC   (Arabidopsis thaliana) centromere. The constructs are useful for
CC   producing stably inherited michrosomes which can serve as vectors for
CC   the construction of transgenic plant and animal cells expressing
CC   selected proteins such as hormones, enzymes, interleukins, clotting
CC   factors, cytokines, antibodies, and growth factors.
XX
SQ   Sequence 611590 BP; 181893 A; 124460 C; 120254 G; 184983 T; 0 other;

  Query Match             73.8%;  Score 19.2;  DB 21;  Length 611590;
  Best Local Similarity   87.5%;  Pred. No. 1.4e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3 TCCCCAAATCAATTACATTTTCTC 26
           |||||||||| ||| |||| ||||
Db   61533 TCCCCAAATCGATTTCATTATCTC 61556


RESULT 8
AAS46283/c
ID   AAS46283 standard; DNA; 6591 BP.
XX
AC   AAS46283;
XX
DT   18-DEC-2001  (first entry)
XX
DE   Tumour suppressor gene derived chemically modified sequence #5.
XX
KW   Human; tumour suppressor gene; oncogene; antitumour; cytostatic;
KW   cancer; tumour; CpC dinucleotide; single-nucleotide polymorphism, SNP;
KW   cytosine methylation; ds.
XX
OS   Homo sapiens.
XX
PN   WO200168912-A2.
XX
PD   20-SEP-2001.
XX
PF   15-MAR-2001; 2001WO-EP02955.
XX
PR   15-MAR-2000; 2000DE-1013847.
PR   06-APR-2000; 2000DE-1019058.
PR   07-APR-2000; 2000DE-1019173.
PR   30-JUN-2000; 2000DE-1032529.
PR   01-SEP-2000; 2000DE-1043826.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A, Piepenbrock C, Berlin K;
XX
DR   WPI; 2001-602752/68.
XX
PT   Fragments of chemically modified genes associated with tumour suppressor
PT   genes and oncogenes, useful in designing primers and probes for
PT   analysing diseases associated with cytosine methylation state e.g.
PT   cancer -
XX
PS   Claim 1, SEQ ID No 5, 27pp; English.
XX
CC   The invention relates to a nucleic acid comprising a sequence of 18
CC   bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with
CC   bisulphite, of genes associated with tumour suppression and
CC   oncogenes having a sequence taken from 536 (actually 533 since
CC   numbers 408, 458 and 500 are missing from the sequence listing) sequences
CC   (Ss) and sequences complementary to (Ss). The nucleic acid may be a
CC   peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may
CC   form part of a set of probes for detecting the cytosine methylation state
CC   and/or single nucleotide polymorphisms and also to be used in an
CC   array for analysing diseases associated with CpG dinucleotides e.g.
CC   cancers and tumours. The probes can also be used in a method for
CC   ascertaining genetic and/or epigenetic parameters for the diagnosis
CC   and/or therapy of existing diseases or the predisposition to specific
CC   diseases, by analysing cytosine methylations. The parameters may be
CC   compared to another set of genetic and/or epigenetic parameters, the
CC   differences serving as basis for diagnosis and/or prognosis events which
CC   are disadvantageous to patients. The present sequence is one of the
CC   533 genomic sequences derived from tumour suppressor genes and
CC   oncogenes.
CC   Note: The sequence data for this patent did not form part
CC   of the printed specification, but was obtained in electronic
CC   format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 6591 BP; 1575 A; 276 C; 1635 G; 3105 T; 0 other;

  Query Match             73.1%;  Score 19;  DB 22;  Length 6591;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CCTCCCCAAATCAATTACA 19
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Db    6247 CCTCCCCAAATCAATTACA 6229


RESULT 9
AAK78476/c
ID   AAK78476 standard; DNA; 3912 BP.
XX
AC   AAK78476;
XX
DT   07-NOV-2001  (first entry)
XX
DE   Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33268.
XX
KW   Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW   cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS   Homo sapiens.
XX
PN   WO200157182-A2.
XX
PD   09-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US01354.
XX
PR   31-JAN-2000; 2000US-0179065.
PR   04-FEB-2000; 2000US-0180028.
PR   24-FEB-2000; 2000US-0184664.
PR   02-MAR-2000; 2000US-0186350.
PR   16-MAR-2000; 2000US-0189874.
PR   17-MAR-2000; 2000US-0190076.
PR   18-APR-2000; 2000US-0198123.
PR   19-MAY-2000; 2000US-0205515.
PR   07-JUN-2000; 2000US-0209467.
PR   28-JUN-2000; 2000US-0214886.
PR   30-JUN-2000; 2000US-0215135.
PR   07-JUL-2000; 2000US-0216647.
PR   07-JUL-2000; 2000US-0216880.
PR   11-JUL-2000; 2000US-0217487.
PR   11-JUL-2000; 2000US-0217496.
PR   14-JUL-2000; 2000US-0218290.
PR   26-JUL-2000; 2000US-0220963.
PR   26-JUL-2000; 2000US-0220964.
PR   14-AUG-2000; 2000US-0224518.
PR   14-AUG-2000; 2000US-0224519.
PR   14-AUG-2000; 2000US-0225213.
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PR   14-AUG-2000; 2000US-0225266.
PR   14-AUG-2000; 2000US-0225267.
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PR 14-AUG-2000; 2000US-0225268.
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PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
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PR 22-AUG-2000; 2000US-0227182.
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PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
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PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
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PR 13-OCT-2000; 2000US-0239845.
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PR 20-OCT-2000; 2000US-0240960.
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PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
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PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
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PR 17-NOV-2000; 2000US-0249209.
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PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-483426/52.
XX
PT Nucleic acids encoding human immune/haematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
XX
PS Disclosure; SEQ ID NO 33288; 3071pp + Sequence Listing, English.
XX
CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 3912 BP, 1207 A, 695 C, 774 G, 1236 T; 0 other;

Query Match 72.3%, Score 18.8, DB 22, Length 3912;

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  Best Local Similarity   90.9%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 CCTCCCCAAATCAATTACATTT 22
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Db     695 CCTACCCAAAGCAATTACATTT 674


RESULT 10
AAK78477/c
ID   AAK78477 standard; DNA; 4322 BP.
XX
AC   AAK78477;
XX
DT   07-NOV-2001  (first entry)
XX
DE   Human immune/haematopoietic antigen genomic sequence SEQ ID NO:35289.
XX
KW   Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW   cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS   Homo sapiens.
XX
PN   WO200157182-A2
XX
PD   09-AUG-2001
XX
PF   17-JAN-2001; 2001WO-US01354
XX
PR   31-JAN-2000; 2000US-0179065
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PR   24-FEB-2000; 2000US-0184664
PR   02-MAR-2000; 2000US-0186350
PR   16-MAR-2000; 2000US-0189874
PR   17-MAR-2000; 2000US-0190076.
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PP   29-SEP-2000; 2000US-0236370.
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PP   20-OCT-2000; 2000US-0241785.
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PR   01-NOV-2000; 2000US-0244617.
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PR   08-NOV-2000; 2000US-0246478.
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PR   08-NOV-2000; 2000US-0246528.
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PP   17-NOV-2000; 2000US-0249208.
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PR   17-NOV-2000; 2000US-0249216.
PR   17-NOV-2000; 2000US-0249217.
PR   17-NOV-2000; 2000US-0249218.
PR   17-NOV-2000; 2000US-0249244.
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PR   17-NOV-2000; 2000US-0249245.
PR   17-NOV-2000; 2000US-0249264.
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PR   17-NOV-2000; 2000US-0249300.
PR   01-DEC-2000; 2000US-0250160.
PR   01-DEC-2000; 2000US-0250391.
PR   05-DEC-2000; 2000US-0251030.
PR   05-DEC-2000; 2000US-0251988.
PR   05-DEC-2000; 2000US-0252719.
PR   06-DEC-2000; 2000US-0251479.
PR   08-DEC-2000; 2000US-0251856.
PR   08-DEC-2000; 2000US-0251868.
PR   08-DEC-2000; 2000US-0251869.
PR   08-DEC-2000; 2000US-0251989.
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PR   11-DEC-2000; 2000US-0254097.
PR   05-JAN-2001; 2001US-0259678.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Barash SC,  Ruben SM;
XX
DR   WPI; 2001-484426/52.
XX
PT   Nucleic acids encoding human immune/haematopoietic antigen polypeptides,
PT   useful for preventing, diagnosing and/or treating cancers and
PT   metastasis
XX
PS   Disclosure; SEQ ID NO 33283; 357pp + Sequence Listing; English
XX
CC   AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC   amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC   activity, and can be used in gene therapy and vaccine production. (I)
CC   proteins and polynucleotides may be used in the prevention, diagnosis and
CC   treatment of diseases associated with inappropriate (I) expression. For
CC   example, they may be used to treat disorders associated with decreased
CC   expression by rectifying mutations or deletions in a patient's genome
CC   that affect the activity of (I) by expressing inactive proteins or to
CC   supplement the patients own production of (I). Additionally, (I)
CC   polynucleotides may be used to produce the secreted (I), by inserting
CC   the nucleic acids into a host cell and culturing the cell to express the
CC   protein. (I) proteins and polynucleotides may be used to prevent,
CC   diagnose and treat immune/haematopoietic related diseases, especially
CC   cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC   to AAK87694 represent human immune/haematopoietic antigen genomic
CC   sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC   represent sequences used in the exemplification of the present invention.
XX
SQ   Sequence 4322 BP; 1435 A; 761 C; 857 G; 1367 T; 0 other;

  Query Match             72.3%;  Score 18.8;  DB 22;  Length 4322;
  Best Local Similarity   90.9%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 CCTCCCCAAATCAATTACATTT 22
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Db     695 CCTACCCAAAGCAATTACATTT 674


RESULT 11
ABK39921/c
ID   ABK39921 standard; DNA; 17869 BP.
XX
AC   ABK39921;
XX
DT   21-MAY 2002  (first entry)
XX
DE   Human chemically pretreated gene sequence #1 strand 2.
XX
KW   Human; ds; bisulphite treatment; CpG; DNA methylation; cancer; tumour;
KW   cytostatic, ALDH6, CYP11A, CYP11B1, CYP3A3, DPYD, EPHX2, OCLN, TXNRD1,
KW   UGT8, MRP, pharmacogenomics, SNP, single nucleotide polymorphism.
XX
OS   Homo sapiens.
XX
PN   WO200202806-A2.
XX
PD   10 JAN 2002.
XX
PF   29-JUN-2001; 2001WO-EP07470.
XX
PR   30-JUN-2000; 2000DE-1032529.
PR   01-SEP-2000; 2000DE-1043826.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2002-154757/20.
XX
PT   New nucleic acid, oligonucleotides and peptide nucleic acid-oligomers,
PT   useful for detecting cytosine methylation state of genes associated
PT   with pharmacogenomics and for therapy of diseases e.g. cancer
XX
PS   Claim 1; SEQ ID No 2; 24pp; English.
XX
CC   The invention relates to a nucleic acid comprising a sequence at
CC   least 18 bases in length of a segment of the chemically pretreated DNA
CC   of genes associated with pharmacogenomics according to one of the
CC   sequences of the genes ALDH6 (NM_000691), CYP11A (NM_000781), CYP11B1
CC   (NM_000497), CYP3A3 (NM_000776 and NM_017460), DPYD (NM_000110), EPHX2
CC   (NM_001979), OCLN (NM_002538), TXNRD1 (NM_003330), UGT8 (NM_003360),
CC   MRP (NM_004996, NM_019900, NM_019901, NM_019902, NM_019862, NM_019898,
CC   NM_019899) and their complementary sequences, or a sequence (S1) chosen
CC   from 87 sequences and their complements. The chemical pretreatment
CC   is bisulphite treatment to convert cytosines (but not methyl cytosines)
CC   into uracils. Also included are an oligomer (II) in particular an
CC   oligonucleotide or a peptide nucleic acid (PNA)-oligomer, comprising in
CC   each case at least one base sequence having a length of 9 nucleotides
CC   which hybridises to or is identical to a chemically pretreated DNA of
CC   genes associated with pharmacogenomics and their complements, arranged in
CC   an array for analysing diseases associated with the methylation state
CC   (CpG) and/or detecting SNPs (single nucleotide polymorphisms)
CC   of the 87 sequences. The oligomers may also be used as PCR primers.
CC   The set of 87 nucleic acids and their complements is useful for diagnosis
CC   and therapy of solid tumours and cancer. The present sequence
CC   represents one the 87 DNA sequences or its complement.
CC   Note: The sequence data for this patent did not form part
CC   of the printed specification, but was obtained in electronic
CC   format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 17869 BP; 5366 A; 158 C; 3365 G; 8978 T; 2 other;

  Query Match             72.3%;  Score 18.8;  DB 24;  Length 17869;
  Best Local Similarity   90.9%;  Pred. No. 1.7e+02;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3 TCCCCAAATCAATTACATTTTC 24
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Db   12020 TCCCAAAATCTATTACATTTTC 11999


RESULT 12
ABL32105/c
ID   ABL32105 standard; DNA; 17869 BP.
XX
AC   ABL32105;
XX
DT   26 MAR 2002  (first entry)
XX
DE   Human immune system associated gene SEQ ID NO: 78.
XX
KW   Human; immune system disease; cytosine methylation; antiasthmatic;
```

KW antiarteriosclerotic; antianaemic; cytostatic; nootropic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia, Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
KW gene; ds.
XX
OS Homo sapiens
XX
PN WO200200928 A2.
XX
PD 03-JAN-2002.
XX
PF 02-JUL-2001; 2001WO-EP07537.
XX
PR 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2002-130909/17.
XX
PT Nucleic acid comprising fragment of chemically modified gene, useful
PT for diagnosis and treatment of diseases associated with abnormal
PT cytosine methylation -
XX
PS Claim 1; SEQ ID NO 78; 32pp + Sequence Listing; German.
XX
CC The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention.
XX
SQ Sequence 17869 BP; 5366 A; 158 C; 3365 G; 8978 T; 2 other;

Query Match 72.3%; Score 18.8; DB 24; Length 17869;
Best Local Similarity 90.9%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TCCCCAAATCAATTACATTTTC 24
||||| ||||| |||||||||||
Db 12020 TCCCAAAATCTATTACATTTTC 11999

RESULT 13
ABK78300/c
ID ABK78300 standard; DNA; 371 BP.
XX
AC ABK78300;
XX
DT 13-AUG-2002 (first entry)
XX
DE Bacillus clausii genomic sequence tag (GST) #1143.
XX
KW Differential gene expression; genomic sequenced tag; GST;
KW altered culture condition; environmental stress;
KW physiological provocation; ds.
XX
OS Bacillus clausii.
XX
PN WO200229113-A2.
XX
PD 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US31437.
XX
PR 06-OCT-2000; 2000US-0680598.
PR 27-MAR-2001; 2001US-279526P.
XX
PA (NOVO) NOVOZYMES BIOTECH INC.
PA (NOVO) NOVOZYMES AS.
XX
PI Berka R, Clausen IG;
XX
DR WPI; 2002-416684/44.
XX
PT Monitoring differential expression of several genes in first Bacillus
PT cell relative to expression of same genes in one or more second
PT Bacillus cells, by using substrate containing Bacillus genomic
PT sequenced tag array -
XX
PS Claim 11; SEQ ID NO 5591; 200pp; English.
XX
CC The invention describes a method of monitoring differential expression of
CC genes in a first Bacillus cell relative to expression of the genes in
CC other Bacillus cells, comprising hybridising labelled nucleic acid probes
CC isolated from Bacillus cells to a substrate containing array of Bacillus
CC genomic sequenced tags (GST), examining the array, and determining
CC relative gene expression by an observed hybridisation reporter signal of
CC a spot in the array. The method is useful for measuring the expression of
CC genes in a first Bacillus cell relative to expression of the same genes
CC in one or more second Bacillus cells. The method is useful for monitoring
CC global expression of several genes from a Bacillus cell, discovering new
CC genes, identifying possible functions of unknown open reading frames and
CC monitoring gene copy number variation and stability. Monitoring changes
CC in expression of genes may be used to provide a representation of the way
CC in which Bacillus cells adapt to changes in culture conditions,
CC environmental stress or other physiological provocation. Extensive
CC follow-up characterisation is unnecessary, when one spot on an array
CC equals one gene or one open reading frame, since sequence information is
CC available. This sequence represents a genomic sequence tag (GST) used in
CC the method of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 371 BP; 101 A; 68 C; 87 G; 106 T; 9 other;

Query Match 71.5%; Score 18.6; DB 24; Length 371;
Best Local Similarity 84.0%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CCTCCCCAAATCAATTACATTTTCT 25
|| | |||| |||| ||||||||||
Db 279 CCACTCCAAGTCAAATACATTTTCT 255

RESULT 14
AAF09771
ID AAF09771 standard; cDNA; 628 BP.
XX
AC AAF09771;
XX
DT 13-MAR-2001 (first entry)
XX
DE Fusarium venenatum EST SEQ ID NO:2294.
XX
KW Multiple gene expression; filamentous fungal cell; EST;
KW expressed sequence tag; Fusarium venenatum; Aspergillus niger;
KW Aspergillus oryzae; Trichoderma reesei, identification, recombination;
KW culture condition; environmental stress; spore morphogenesis;
KW metabolic pathway engineering; catabolic pathway engineering; ss.
XX
OS Fusarium venenatum.
XX
PN WO200056762-A2.
XX
PD 28-SEP-2000.

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XX
PF   22-MAR-2000; 2000WO-US07781.
XX
PR   22-MAR-1999;   99US-0273623.
XX
PA   (NOVO ) NOVO NORDISK BIOTECH INC.
PA   (NOVO ) NOVO NORDISK AS.
XX
PI   Berka RM,  Rey MW,  Shuster JR,  Kauppinen S,  Clausen IG,  Olsen PB;
XX
DR   WPI; 2000-594572/56.
XX
PT   Monitoring differential expression of genes in filamentous fungal cells
PT   uses fluorescence labeled nucleic acids isolated from the cells and a
PT   substrate of expressed sequence tags -
XX
PS   Claim 86; Page 1240; 816pp; English.
XX
CC   The present invention describes a method for monitoring differential
CC   expression of genes in a first filamentous fungal (FF) cell relative to
CC   expression of the same genes in one or more second filamentous fungal
CC   cells. The method uses fluorescence labeled nucleic acids isolated from
CC   the FF cells and a substrate of expressed sequence tags (ESTs). The ESTs
CC   are used in the methods for monitoring differential expression of genes
CC   in a first filamentous fungal (FF) cell relative to expression of the
CC   same genes in one or more second filamentous fungal cells. Monitoring
CC   the global expression of genes from FF cells allows the production
CC   potential of the microorganisms to be improved. New genes may be
CC   discovered, possible functions of unknown open reading frames can be
CC   identified and gene copy number variation and stability can be
CC   monitored. The expression of genes can be used to study how FF cells
CC   adapt to changes in culture conditions, environmental stress, spore
CC   morphogenesis, recombination, metabolic or catabolic pathway
CC   engineering. Using ESTs provides several advantages over genomic or
CC   random cDNA clones including elimination of redundancy as one spot on an
CC   array equals one gene or open reading frame, and organisation of the
CC   microarrays based on function of the gene products to facilitate
CC   analysis of the results. AAF07478 to AAF11247 represents ESTs from
CC   Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus
CC   niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and
CC   AAF14879 to AAF15437 represents ESTs from Trichoderma reesei, which are
CC   all specifically claimed in the present invention.
XX
SQ   Sequence 628 BP; 148 A; 197 C; 101 G; 172 T; 10 other;

  Query Match             71.5%;  Score 18.6;  DB 21;  Length 628;
  Best Local Similarity   84.0%;  Pred. No. 1.6e+02;
  Matches   21;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 CCTCCCCAAATCAATTACATTTTCT 25
           ||||||  ||||||  ||  ||  |||||
Db     294 CCTCCCAAAATCACTTCCAGTTTCT 317


RESULT 15
ABL29546
ID   ABL29546 standard; DNA; 2984 BP.
XX
AC   ABL29546;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster genomic polynucleotide SEQ ID NO 40111.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical; gene; ds.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US09231.
XX
PR   23-MAR-2000; 2000US-191637P.
PR   11-JUL-2000; 2000US-0614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signalling and cell cell
PT   interactions -
XX
PS   Claim 1; SEQ ID NO 40111; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins
CC   (ABB57737-ABB72072).
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 2984 BP; 853 A; 601 C; 631 G; 899 T; 0 other;

  Query Match             71.5%;  Score 18.6;  DB 23;  Length 2984;
  Best Local Similarity   84.0%;  Pred. No. 1.8e+02;
  Matches   21;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2 CTCCCCAAATCAATTACATTTTCTC 26
           ||||  | ||  ||||||||||||||
Db    2198 CTCCTTAGATTAATTACATTTTGTC 2220


Search completed: January 14, 2003, 11:54:17
Job time : 107.296 secs
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